

A framework human-mouse comparative map was constructed from orthologs mapped in both mouse and in a YAC-based STS-content map of human chromosome 7. In addition to this traditional approach, human-mouse orthologs mapped in mouse but not included in the human STS-content map were integrated into the map based on sequence alignment to ordered human genomic sequence (*). The location of genes at the end of conserved segments is indicated by the corresponding or closest STS (sWSS) marker. Genes, designated with the human gene symbol when available, included in the map are color coded and shown to the right. Chromosome and map location for mouse genes shown are from the Mouse Genome Database (<http://www.informatics.jax.org>). Origin of the mouse genes in the map are represented by the following symbols: ^a, from the Mouse Genome Database (<http://www.informatics.jax.org>) comparative mapping database; ^b, genetically mapped on The Jackson Laboratory interspecific backcross panel (C57BL/6Jei x SPRET/Ei)F₁ x SPRET/Ei (The Jackson Laboratory BSS backcross panel); ^c, cytogenetically mapped (L.A. Everett and E.D. Green, unpublished, ^{cu}); ^d, from the Mouse Genome Database (<http://www.informatics.jax.org>); ^e, literature based; ^f, Davis Human/Mouse Homology Map (<http://www.ncbi.nlm.nih.gov/Homology>). One gene in the HOXA@ cluster was mapped to the STS-map while the other 10 HOX genes were included based on sequence alignment. One marker on the map is not a traditional gene, *Iapls2-2*, but was included based on non-repetitive sequence similarity to human genomic sequence. The size of the human chromosome 7 YAC contigs are drawn to scale.